



SEQUENCE LISTING

<110> Munroe, Donald
Gupta, Ashwani
Vyas, Tejal
Chun, Jerold

<120> MAMMALIAN EDG-5 RECEPTOR HOMOLOGS

<130> 2931-105 (new); P108074-00003 (old)

<140> US 09/581252
<141> 2000-12-04

<150> PCT/CA 98/01193
<151> 1998-12-24

<150> US 08/997803
<151> 1997-12-24

<160> 28

<170> PatentIn version 3.2

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<223> Murine edg-5 RT-PCR clone 501

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37

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 <213> Artificial Sequence

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 <223> PCR primer: JC501-R

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<210> 6
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<210> 12
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 <212> DNA
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 <223> Nucleotide sequence of the genomic DNA flanking 5' end of the
 hedg-5 cDNA insert of pC3-hedg-55 clone and the hedg-5 cDNA

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agaaccacaga gaggcgtccc tctcgcatcc cctccacagt cctcagcagg agtgacacag	1260
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tgctgcattt agagaaagca cag	1523

<210> 13
 <211> 1357
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Nucleotide sequence of a hEDG-5 cDNA inserted into pcDNA3

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gaattcgcgg ccgcgctcgac gttcacttct ccacaatgaa tgagtgtcac tatgacaagc	60
acatggactt tttttataat aggagcaaca ctgatactgt cgatgactgg acaggaacaa	120
agcttgtgat tgttttgtgt gttgggacgt ttttctgcct gtttattttt ttttctaatt	180
ctctgggtcat cgcggcagtg atcaaaaaca gaaaatttca tttccccttt tactacctgt	240
tggctaattt agctgctgcc gatttcttcg ctggaattgc ctatgtattc ctgatgttta	300

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acacaggccc agtttcaaaa actttgactg tcaaccgctg gtttctccgt caggggcttc 360
tggacagtag cttgactgct tccctcacca acttgctggt tatcgccgtg gagaggcaca 420
tgtcaatcat gaggatgctg gtccatagca acctgaccaa aaagaggggtg aactgctca 480
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<210> 14

<211> 353

<212> PRT

<213> Artificial Sequence

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<223> Predicted amino acid sequence of pC3-hedg5-3 clone

<400> 14

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Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
1           5           10           15

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Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
          20           25           30

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Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
 35 40 45
 Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
 50 55 60
 Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly
 65 70 75 80
 Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
 85 90 95
 Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
 100 105 110
 Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
 115 120 125
 Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
 130 135 140
 Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
 145 150 155 160
 Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
 165 170 175
 Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
 180 185 190
 Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
 195 200 205
 Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
 210 215 220
 Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
 225 230 235 240
 Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
 245 250 255

Val Val Leu Pro Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
305 310 315 320

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325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr
340 345 350

Ser

<210> 15

<211> 213

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted amino acid sequence of mouse partial EDG-5 cDNA

<220>

<221> MISC_FEATURE

<222> (188)..(210)

<223> Xaa = unknown

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Arg Gln Gly Leu Leu Asp Thr Ser Leu Thr Ala Ser Leu Ala Asn Leu
20 25 30

Leu Val Ile Ala Val Glu Arg His Met Ser Ile Met Arg Met Arg Val

35

40

45

His Ser Asn Leu Thr Lys Lys Arg Val Thr Leu Leu Ile Leu Leu Val
50 55 60

Trp Ala Ile Ala Ile Phe Met Gly Ala Val Pro Thr Leu Gly Trp Asn
65 70 75 80

Cys Leu Cys Asn Ile Ser Ala Cys Ser Ser Leu Ala Pro Ile Tyr Ser
85 90 95

Arg Ser Tyr Leu Ile Phe Trp Thr Val Ser Asn Leu Leu Ala Phe Phe
100 105 110

Ile Met Val Ala Val Tyr Val Arg Ile Tyr Met Tyr Val Lys Arg Lys
115 120 125

Thr Asn Val Leu Ser Pro His Thr Ser Gly Ser Ile Ser Arg Arg Arg
130 135 140

Ala Pro Met Lys Leu Met Lys Thr Val Met Thr Val Leu Gly Ala Phe
145 150 155 160

Val Val Cys Trp Thr Pro Gly Leu Val Val Leu Leu Leu Asp Gly Leu
165 170 175

Asn Cys Lys Gln Cys Asn Val Gln His Val Lys Xaa Trp Phe Leu Leu
180 185 190

Leu Ala Leu Leu Asn Ser Val Met Asn Pro Leu Ile Tyr Cys Arg Ser
195 200 205

Pro Xaa Phe Pro Trp
210

<210> 16
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<212> DNA
<213> Artificial Sequence

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<210> 17
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> PCR primer: HE5-1011R

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<210> 18
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<210> 19
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 <213> Artificial Sequence

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 <223> PCR primer: HE5-1322R

<400> 19
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<210> 20
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 <212> DNA
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 <223> PCR primer: HE5-KZKF

<400> 20
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<210> 21
 <211> 39
 <212> DNA

<213> Artificial Sequence

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<223> PCR primer: HE5-Kpn1322R

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39

<210> 22

<211> 2033

<212> DNA

<213> Artificial Sequence

<220>

<223> Full length mEDG-5 cDNA

<400> 22

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aacaggagca acacagacac agcggacgag tggacaggga caaagcttgt gatcgtcctg 120

tgcgtgggga cgttcttctg cctctttata ttttttctta actccctggg cattgctgcg 180

gtgatcacia accggaagtt ccactttccc ttctactacc tgctggctaa cttagctgct 240

gcggatttct tcgccggaat cgcttacgtg ttctgatgt ttaacactgg cccggtgtcg 300

aaaacgttga ccgtcaaccg ctggttcctc cgccaggggc tcctagacac cagcctgact 360

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agagtccaca gcaacttgac caaaaagcgg gtgacgctgc tcattctgct ggtgtgggcc 480

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gcctgctctt ctctggctcc catttacagt aggagttacc tcattttctg gactgtgtcc 600

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aggaaaacca acgtcttata tccacacacc agtggctcca tcagccgccg gagggctccc 720

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 <211> 354
 <212> PRT
 <213> Mouse

<400> 23

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 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Thr Asn Arg Lys Phe His Phe Pro
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Ala Asp Phe Phe Ala Gly
65 70 75 80
Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
85 90 95
Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Thr Ser
100 105 110
Leu Thr Ala Ser Leu Ala Asn Leu Leu Val Ile Ala Val Glu Arg His
115 120 125
Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
130 135 140
Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
145 150 155 160
Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
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Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Ile Phe Trp Thr
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Val Ser Asn Leu Leu Ala Phe Phe Ile Met Val Ala Val Tyr Val Arg
195 200 205
Ile Tyr Met Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
210 215 220
Ser Gly Ser Ile Ser Arg Arg Arg Ala Pro Met Lys Leu Met Lys Thr
225 230 235 240
Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
245 250 255
Val Val Leu Leu Leu Asp Gly Leu Asn Cys Lys Gln Cys Asn Val Gln
260 265 270
His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Met
275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Asn Thr Met
 290 295 300

Arg Lys Met Ile Cys Cys Ala Leu Gln Asp Ser Asn Thr Glu Arg Arg
 305 310 315 320

Pro Ser Arg Asn Pro Ser Thr Ile His Ser Arg Ser Glu Thr Gly Ser
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Gln Tyr Leu Glu Asp Ser Ile Ser Gln Gly Pro Val Cys Asn Lys Asn
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Gly Ser

<210> 24
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 <212> DNA
 <213> Artificial Sequence

<220>
 <223> cDNA sequence of clone pC3-hEDG5#3.4 from the region encoding a
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<210> 25

<211> 1062

<212> DNA

<213> Artificial Sequence

<220>

<223> cDNA sequence of clone pC3-hEDG5#28 from the region encoding a hEDG5 polypeptide

<400> 25

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ctggcgctgc tcaactccgt cgtgaacccc atcatctact cctacaagga cgaggacatg	900
tatggcacca tgaagaagat gatctgctgc ttctctcagg agaaccaga gaggcgtccc	960

tctcgcaccc cctccacagt cctcagcagg agtgacacag gcagccagta catagaggat 1020
 agtattagcc aaggtgcagt ctgcaataaa agcacttcct aa 1062

<210> 26
 <211> 1523
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Complementary strand nucleotide sequence of the genomic DNA
 flanking 5' end of the hedg-5 cDNA insert of pC3-hedg-55 clone
 and the hedg-5 cDNA

<400> 26
 gtggaaggat tggactcgcc ggatcggacc ctttgtttgt taattttaca cgcgatttac 60
 gacaccatcc tccagtcccc gatacaggac ctggtttcct gtaaactga ctctggactg 120
 tgaagtccag aagttgaggg aactaccctc aatcgggtctt gcccgaaatct ttgtcgttaa 180
 ctaccgaatc actgactaaa atgtttacta taaacaaaga agaaatttaa agaaagatcc 240
 tacaagtga gaagaggtgt tacttactca cagtgatact gttcgtgtac ctgaaaaaaaa 300
 tattatcctc gttgtgacta tgacagctac tgacctgtcc ttgtttcgaa cactaacaaa 360
 acacacaacc ctgcaaaaag acggacaaat aaaaaaaaaag attaagagac cagtagcgcc 420
 gtcactagtt tttgtctttt aaagtaaagg ggaaaatgat ggacaaccga ttaaactgcac 480
 gacggctaaa gaagcgacct taacggatac ataaggacta caaattgtgt ccgggtcaaa 540
 gtttttgaaa ctgacagttg gcgaccaaag aggcagtccc cgaagacctg tcatcgaact 600
 gacgaaggga gtggttgaac gaccaatagc ggcacctctc cgtgtacagt tagtactcct 660
 acgcccaggt atcgttggac tggtttttct cccactgtga cgagtaaaac gaacagaccc 720
 ggtagcggta aaaatacccc cgccaggggt gtgacccgac cttaacggag acgttgtaga 780
 gacggacgag aagggaccgg gggtaaagtgt cgtcctcaat ggaacaaaag acctgtcaca 840
 ggttgagta ccggaaggag tagtaccac accacatgga cgcctagatg cacatgcagt 900
 tctccttttg gttgcagaac agaggcgtat gttcacccag gtagtcggcg gcctcctgtg 960
 ggtacttcga ttacttctgc cactactgac agaatccccg caaacacat acgacctggg 1020
 gcccggaaca ccaagacggg gagctgccgg acttgacgtc cgtcacaccg cacgtcgtac 1080
 acttttccac caaggacgac gaccgcgacg agttgaggca gcacttgggg tagtagatga 1140
 ggatgttcct gctcctgtac ataccgtggt acttcttcta ctagacgacg aagagagtcc 1200

tcttggtct ctccgcaggg agagcgtagg ggaggtgtca ggagtcgtcc tcaactgtgtc 1260
 cgtcgggtcat gtatctccta tcataatcgg ttccacgtca gacgttattt tcgtgaagga 1320
 tttgagacct acggagarcc ggggtgggtcc ggaggagacc cttttctcga caattcttac 1380
 taatggacag agattgtttc gggtagatgt cacaataaac tccagaggta attagtgcg 1440
 atctaaagaa attttttaaa aaaaagtatc aaattttcgt acccgtcatt tctctcctgg 1500
 acgacgtaaa tctctttcgt gtc 1523

<210> 27
 <211> 353
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Predicted amino acid sequence of hEDG5 encoded by clone
 pC3-hEDG5#3.4

<400> 27

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
 1 5 10 15

Ser Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
 20 25 30

Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
 35 40 45

Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
 50 55 60

Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly
 65 70 75 80

Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
 85 90 95

Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
 100 105 110

Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
 115 120 125

Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
 130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly
 145 150 155 160

Ala Val Pro Thr Leu Gly Trp Asn Cys Leu Cys Asn Ile Ser Ala Cys
 165 170 175

Ser Ser Leu Ala Pro Ile Tyr Ser Arg Ser Tyr Leu Val Phe Trp Thr
 180 185 190

Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg
 195 200 205

Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr
 210 215 220

Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr
 225 230 235 240

Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu
 245 250 255

Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln
 260 265 270

His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val
 275 280 285

Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met
 290 295 300

Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro
 305 310 315 320

Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln
 325 330 335

Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr

340

345

350

Ser

<210> 28

<211> 353

<212> PRT

<213> Artificial Sequence

<220>

<223> Predicted amino acid sequence of hEDG5 encoded by clone
pC3-hEDG5#28

<400> 28

Met Asn Glu Cys His Tyr Asp Lys His Met Asp Phe Phe Tyr Asn Arg
1 5 10 15Gly Asn Thr Asp Thr Val Asp Asp Trp Thr Gly Thr Lys Leu Val Ile
20 25 30Val Leu Cys Val Gly Thr Phe Phe Cys Leu Phe Ile Phe Phe Ser Asn
35 40 45Ser Leu Val Ile Ala Ala Val Ile Lys Asn Arg Lys Phe His Phe Pro
50 55 60Phe Tyr Tyr Leu Leu Ala Asn Leu Ala Ala Asp Phe Phe Ala Gly
65 70 75 80Ile Ala Tyr Val Phe Leu Met Phe Asn Thr Gly Pro Val Ser Lys Thr
85 90 95Leu Thr Val Asn Arg Trp Phe Leu Arg Gln Gly Leu Leu Asp Ser Ser
100 105 110Leu Thr Ala Ser Leu Thr Asn Leu Leu Val Ile Ala Val Glu Arg His
115 120 125Met Ser Ile Met Arg Met Arg Val His Ser Asn Leu Thr Lys Lys Arg
130 135 140

Val Thr Leu Leu Ile Leu Leu Val Trp Ala Ile Ala Ile Phe Met Gly

145		150		155		160
Ala Val Pro Thr	Leu Gly Trp Asn Cys	Leu Cys Asn Ile Ser	Ala Cys			
	165	170	175			
Ser Ser Leu Ala Pro Ile Tyr Ser	Arg Ser Tyr Leu Val Phe Trp Thr					
	180	185	190			
Val Ser Asn Leu Met Ala Phe Leu Ile Met Val Val Val Tyr Leu Arg						
	195	200	205			
Ile Tyr Val Tyr Val Lys Arg Lys Thr Asn Val Leu Ser Pro His Thr						
	210	215	220			
Ser Gly Ser Ile Ser Arg Arg Arg Thr Pro Met Lys Leu Met Lys Thr						
	225	230	235			240
Val Met Thr Val Leu Gly Ala Phe Val Val Cys Trp Thr Pro Gly Leu						
	245	250	255			
Val Val Leu Leu Leu Asp Gly Leu Asn Cys Arg Gln Cys Gly Val Gln						
	260	265	270			
His Val Lys Arg Trp Phe Leu Leu Leu Ala Leu Leu Asn Ser Val Val						
	275	280	285			
Asn Pro Ile Ile Tyr Ser Tyr Lys Asp Glu Asp Met Tyr Gly Thr Met						
	290	295	300			
Lys Lys Met Ile Cys Cys Phe Ser Gln Glu Asn Pro Glu Arg Arg Pro						
	305	310	315			320
Ser Arg Ile Pro Ser Thr Val Leu Ser Arg Ser Asp Thr Gly Ser Gln						
	325	330	335			
Tyr Ile Glu Asp Ser Ile Ser Gln Gly Ala Val Cys Asn Lys Ser Thr						
	340	345	350			
Ser						